

FIGURE 1

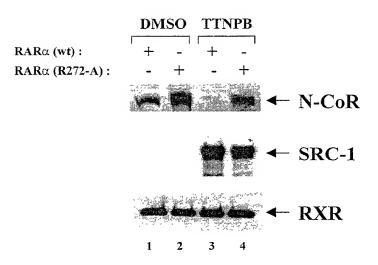


FIGURE 2A

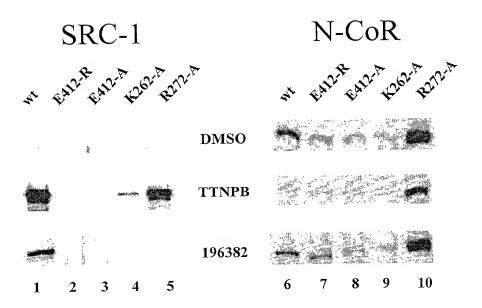


FIGURE 2B

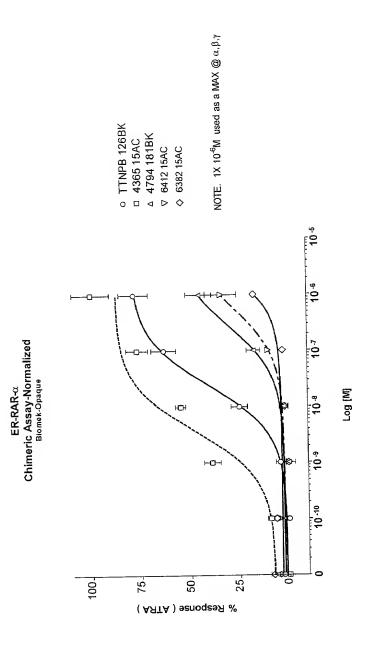


FIGURE 3A

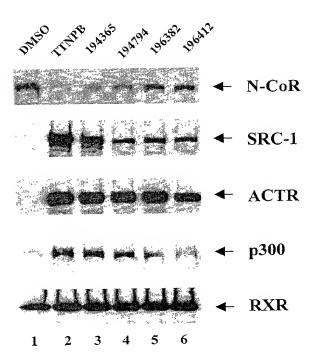


FIGURE 3B

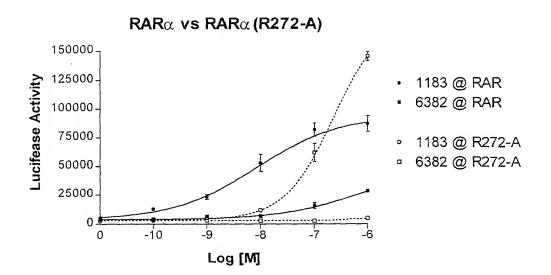


Figure 4

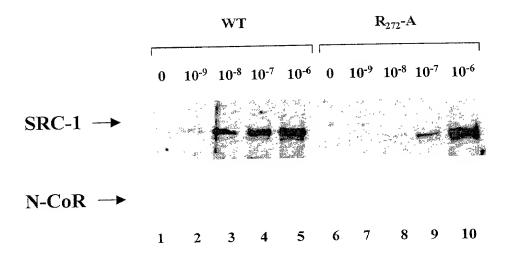


FIGURE 5A

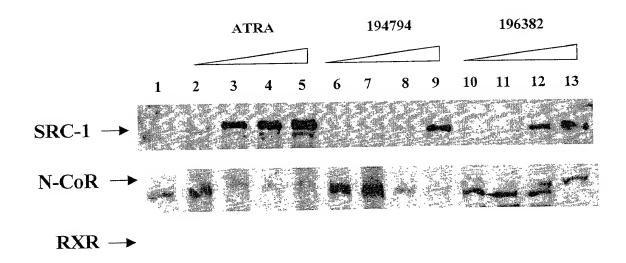
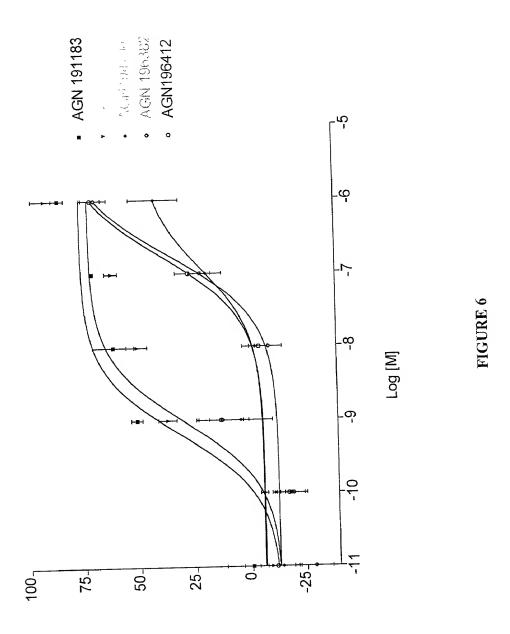


FIGURE 5B



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MASNSSSCPTPGGGHLNGYPVPPYAFFFPPMLGGLSPPGALTTLQHQLPVSGYSTPSPATIE
TQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTC
HRDKNCIINKVTRNRCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGE
LIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVDFAKQLPG
FTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVF
AFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPH
MFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGRDG
GGLAPPPGSCSPSLSPSSNRSSPATHSP

FIGURE 7A

MFDCMDVLSVSPGQILDFYTASPSSCMLQEKALKACFSGLTQTEWQHRHTAQSIETQSTSSE
ELVPSPPSPLPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCV
INKVTRNRCQYCRLQKCFEVGMSKESVRNDRNKKKKETSKQECTESYEMTAELDDLTEKIRK
AHQETFPSLCQLAKYTTNSSADHRVRLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLTIA
DQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFTFANQLL
PLEMDDTETGLLSAICLICGDRQDLEEPTKVDKLQEPLLEALKIYIRKRRPSKPHMFPKILM
KITDLRSISAKGAERVITLKMEIPGSMPPLIQEMMENSEGHEPLTPSSSGNTAEHSPSISPS
SVENSGVSQSPLVQ

FIGURE 7B

MATNKERLFAAGALGPGSGYPGAGFPFAFPGALRGSPPFEMLSPSFRGLGQPDLPKEMASLS
VETQSTSSEEMVPSSPSPPPPPRVYKPCFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKNMVY
TCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSKEAVRNDRNKKKKEVKEEGSPDSYELSPQL
EELITKVSKAHQETFPSLCQLGKYTTNSSADHRVQLDLGLWDKFSELATKCIIKIVEFAKRL
PGFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDL
VFAFAGQLLPLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLQEPLLEALRLYARRRPSQ
PYMFPRMLMKITDLRGISTKGAERAITLKMEIPGPMPPLIREMLENPEMFEDDSSQPGPHPN
ASSEDEVPGGOGKGGLKSPA

FIGURE 7C

Dimer N-terminus AF1 C4 Zn Fingers CTE E1 Contacts h9 (hAXAa) AF2 C-terminus hRXRα hRARY rTRα1 hPPARy $hER\alpha$ hPR GM Ligand binding Domain. 11 - Contact i Han Han DNA Binding Domain: P-Box mh hRXR4 GKHYGVYSTEGGKÖFFKRTVRXDL--TYTTERDNKDGLIDKRORNRTTYTERYOKTTAHEM JFRXR VKHYGVFAJEGGKÖFFKRSVRNNR--KYSTLGKRH DTOKKSRNRTTYTEREQUEREQUEREQUEREQUERE CTE GYHYRCITTEGEKGEFRRIIGXNLHPSYSGKYEGKEVIDKYTRNG OEFREKKIJYGMAJDLYLDGSKRLAKRKLIEENREK HTRB GYHYGYMSÇEĞĞĞĞEFKRSTQGH--NDYN PATMQTIDKARRKÇÇĞĞ RERKTYEVGMAKGG GCHYGVLTEĞSĞKYFFKRAVEĞQ--HNYLGAGRADGIIDKIRRKYÇ PATRYAKTOĞGA (全1) hERa (22) rGR The second α-helices , and E1 Region Heptad 9 (h9) AF2 Domain φφχ**φ**φφ hRXRQ WAKRIPH SELPLODVILL jfRXR WAKRLPH ROLSIAPIVVLL hTRQ1 FAKKLPM SELPCEDDIILL hRARY FAKRLPG TGLSIAPIITLL hPARY YAKSIPO VNLOLNOVTLL $\binom{23}{24}$ LULULEALR VILRIPALR (33)(43)hRXRa FLHEML (34)j FRXR (44) JFRXR FLLDML ${25}$ ${26}$ ${27}$ hTRAI LLMKVTOLR HRAR, MLMKITOLR HPPAR, LLQKNTOLR LECET A hTRa1 hRARY hPPARY $\binom{28}{29}$ (38) (39) MLMKLYSLR **hLXR** HVDR HVDR MIQKLADLR HVDR LVLEYF (30)WAKRYPO VOLTLHOOVHLL WAKAIPO RNLHLOOMTLL WSKSLPO RNLHIOMITLI hER (40) (41) (42) hER hGR hPR her hgr hpr LLLILSHIR (50) (51) LITEML (31)(32)hGR LTKLLDSMH MLXEVI MUSEVI **hPR** LTKLLONLH (52)a-helix 3 a-helix 4 cz-helix10/11 a belix 12

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FIGURE 8